SEQUENCE LISTING

<110> The Chemo-Sero-Therapeutic Research Institute

<120> A DNA coding for merozoite protein of Babesia caballi, a recombinant protein obtained by using said DNA and a use thereof

<130> 661440

<160> 2

<210> 1

<211> 1828

<212> DNA

<213> Babesia caballi

<400> 1

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Val Gly Asp Val Thr Lys Thr Leu Leu Ala Ala Ser Glu Ser Val Asp
                10                  15                  20

TCA GCT GCC AAT GCC TAT ATG ATC AAC AGT GAC ATG AGC GAT TAC TTG          152
Ser Ala Ala Asn Ala Tyr Met Ile Asn Ser Asp Met Ser Asp Tyr Leu
            25                  30                  35

TCG GCT GTG TCT GAC AAC TTC GCC GAG CGC ATT TGC AGT CAG GTC CCT          200
Ser Ala Val Ser Asp Asn Phe Ala Glu Arg Ile Cys Ser Gln Val Pro
        40                  45                  50

AAG GGG AGT AAC TGC AGT GCT TCC GTT AGC GCA TAC ATG AGT CGC TGC          248
Lys Gly Ser Asn Cys Ser Ala Ser Val Ser Ala Tyr Met Ser Arg Cys
 55                  60                  65                  70

GCT AAA CAG GAC TGC CTG ACT CTC CAA AGT CTT AAG TAC CCT CTT GAG          296
Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser Leu Lys Tyr Pro Leu Glu
                75                  80                  85

GCT AAG TAC CAA CCG CTG ACC CTT CCT GAC CCC TAC CAG TTG GAG GCC          344
Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp Pro Tyr Gln Leu Glu Ala
                90                  95                  100

GCA TTT ATA CTC TTC AAG GAG AGT GAC GCT AAT CCG GCC AAT AGC ACT          392
Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala Asn Pro Ala Asn Ser Thr
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GAG AAG CGC TTC TGG ATG CGT TTC AGA AGG GGC AAG AAC CAC AGT TAC        440
Glu Lys Arg Phe Trp Met Arg Phe Arg Arg Gly Lys Asn His Ser Tyr
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TTC CAC GAC TTA GTC TTC AAT CTG CTG GAG AAG AAC GTG ACT CGC GAC        488
Phe His Asp Leu Val Phe Asn Leu Leu Glu Lys Asn Val Thr Arg Asp
135                 140                 145                 150

GCG GAT GCT ACT GAC ATT GAG AAC TTT GCG TCC AGG TAC CTG TAC ATG        536
Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala Ser Arg Tyr Leu Tyr Met
                155                 160                 165

GCC ACG CTT TAC TAC AAG ACG TAC ACG AAT GTT GAT GAG TTC GGT GCT        584
Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn Val Asp Glu Phe Gly Ala
                170                 175                 180

AGC TTC TTT AAC AAG TTG TCT TTC ACT ACT GGG TTG TTC GGC TGG GGC        632
Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr Gly Leu Phe Gly Trp Gly
        185                 190                 195

ATC AAG AGG GCA CTT AAG CAG ATT ATT CGC TCT AAC CTG CCC CTT GAC        680
Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg Ser Asn Leu Pro Leu Asp
    200                 205                 210

ATC GGG ACA GAA CAC AGC GTC AGT CGC CTG CAG CAC ATT ACG AGC AGT        728
Ile Gly Thr Glu His Ser Val Ser Arg Leu Gln His Ile Thr Ser Ser
215                 220                 225                 230

TAC AAG GAT TAC ATG GAT ACG CAG ATT CCT GCA CTG CCC AAG TTT GCG        776
Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro Ala Leu Pro Lys Phe Ala
                235                 240                 245

AAG CGT TTC TCC CTT ATG GTA GTG CAG AGG CTG CTG GCC ACC GTG GCT        824
Lys Arg Phe Ser Leu Met Val Val Gln Arg Leu Leu Ala Thr Val Ala
                250                 255                 260

GGT TAC GTC GAC ACC CCG TGG TAT AAG AAG TGG TAC ATG AAG CTG AAG        872
Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys Trp Tyr Met Lys Leu Lys
                265                 270                 275

AAC TTT ATG GTG AAC AGG GTG TTC ATT CCT ACA AAG AAG TTC TTC AAT        920
Asn Phe Met Val Asn Arg Val Phe Ile Pro Thr Lys Lys Phe Phe Asn
    280                 285                 290

AAG GAA ATT CGT GAG CCT AGT AAG GCA TTA AAA GAA AAG GTG TCA ACC        968
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<210> 2

<211> 458

<212> PRT

<213> Babesia caballi

<400> 2

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Asp Met Ser Asp Tyr Leu Ser Ala Val Ser Asp Asn Phe Ala Glu Arg
            35                  40                  45
Ile Cys Ser Gln Val Pro Lys Gly Ser Asn Cys Ser Ala Ser Val Ser
        50                  55                  60
Ala Tyr Met Ser Arg Cys Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser
65                  70                  75                  80
Leu Lys Tyr Pro Leu Glu Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp
                85                  90                  95
Pro Tyr Gln Leu Glu Ala Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala
                100                 105                 110
Asn Pro Ala Asn Ser Thr Glu Lys Arg Phe Trp Met Arg Phe Arg Arg
                115                 120                 125
Gly Lys Asn His Ser Tyr Phe His Asp Leu Val Phe Asn Leu Leu Glu
                130                 135                 140
Lys Asn Val Thr Arg Asp Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala
145                 150                 155                 160
Ser Arg Tyr Leu Tyr Met Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn
                165                 170                 175
Val Asp Glu Phe Gly Ala Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr
                180                 185                 190
Gly Leu Phe Gly Trp Gly Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg
                195                 200                 205
Ser Asn Leu Pro Leu Asp Ile Gly Thr Glu His Ser Val Ser Arg Leu
                210                 215                 220
Gln His Ile Thr Ser Ser Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro
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      225                     230                     235                     240
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                  245                     250                     255
Leu Leu Ala Thr Val Ala Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys
                  260                     265                     270
Trp Tyr Met Lys Leu Lys Asn Phe Met Val Asn Arg Val Phe Ile Pro
                  275                     280                     285
Thr Lys Lys Phe Phe Asn Lys Glu Ile Arg Glu Pro Ser Lys Ala Leu
      290                     295                     300
Lys Glu Lys Val Ser Thr Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile
      305                     310                     315                     320
Gly Gln Gly Thr Val Asp Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser
                  325                     330                     335
Lys Ala Leu Lys Glu Lys Val Ser Asn Asp Ala Lys Asp Leu Phe Glu
                  340                     345                     350
Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg
                  355                     360                     365
Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Gly Ala Glu Asp
      370                     375                     380
Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Asn
      385                     390                     395                     400
Glu Ile Arg Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu
      405                     410                     415
Ala Asp Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp Phe
      420                     425                     430
Ile Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Ile Arg Lys Val
      435                     440                     445
Ser Thr Glu Ala Asp Asn Leu Leu Glu Lys
      450                     455
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